



SEQUENCE LISTING

<110> Soto, Ana M.
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<120> A NOVEL ANDROGEN-INDUCED SUPPRESSOR OF CELL
PROLIFERATION AND USES THEREOF

<130> MBI-008

<140> US 09/512,581

<141> 2000-02-24

<150> US 60/121,461

<151> 1999-02-24

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<170> PatentIn Ver. 2.0

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FEB 05 2003

TECH CENTER 1600/2900

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B1
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B1

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His	Lys	Ser	Leu	Asp	Pro	Ser	Asn	Leu	Glu	His	Leu	Ile	Thr	Pro	Leu		
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B1
JA

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 Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met Val
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 Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr Arg
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Gln Glu Leu Leu Asp Thr Val Leu Val Asn Leu Val Pro Ala His Lys	
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Asp Leu Ile Leu Glu Leu Tyr Asn Ile Asp Ser His Leu Leu Leu Ser	
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Lys Lys Tyr Ala Leu Gln Ser Ala Ala Gly Lys Asp Ala Ala Lys Gln	
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Pro	Thr	Asp	Gln	Ala	Ile	Arg	Ala	Gly	Leu	Glu	Leu	Leu	Lys	Val	Leu	
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His	Ile	Arg	Ser	Ala	Leu	Leu	Pro	Val	Leu	His	His	Lys	Ser	Lys	Lys	
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Phe	Ser	Ser	Lys	Glu	Thr	Gln	Phe	Ala	Gln	Ile	Phe	Glu	Pro	Leu	His	
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Met Asn Ile Ile Met Ser Lys Ser Thr Thr Tyr Ser Leu Glu Ser Pro			
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 Lys Ile Ser Lys Glu Glu Met Val Arg Arg Leu Lys Met Val Val Lys
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 Leu Asn Leu Ala Leu His Leu Ala Ser Asp Phe Phe Leu Lys His Pro
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gat ata ttt atg ttt ata aca aga cag ttg aag ggg cta gag gat aca Asp Ile Phe Met Phe Ile Thr Arg Gln Leu Lys Gly Leu Glu Asp Thr 105 110 115 120			509
aag agc cca caa ttc aat agg tat ttt tat tta ctt gag aac att gct Lys Ser Pro Gln Phe Asn Arg Tyr Phe Tyr Leu Leu Glu Asn Ile Ala 125 130 135			557
tgg gtc aag tca tat aac ata tgc ttt gag tta gaa gat agc aat gaa Trp Val Lys Ser Tyr Asn Ile Cys Phe Glu Leu Glu Asp Ser Asn Glu 140 145 150			605
att ttc acc cag cta tac aga acc tta ttt tca gtt ata aac aat ggc Ile Phe Thr Gln Leu Tyr Arg Thr Leu Phe Ser Val Ile Asn Asn Gly 155 160 165			653
cac aat cag aaa gtc cat atg cac atg gta gac ctt atg agc tct att His Asn Gln Lys Val His Met His Met Val Asp Leu Met Ser Ser Ile 170 175 180			701
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gta aat ctg gta cct gct cat aag aat tta aac aag caa gca tat gat Val Asn Leu Val Pro Ala His Lys Asn Leu Asn Lys Gln Ala Tyr Asp 205 210 215			797
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Pro Leu Trp Gln Cys Tyr Leu Gly Arg Phe Asn Asp Ile His Val Pro
315 320 325

atc cgc ctg gaa tgt gtg aaa ttt gct agc cat tgt ctc atg aac cat 1181
Ile Arg Leu Glu Cys Val Lys Phe Ala Ser His Cys Leu Met Asn His
330 335 340

cct gat tta gca aaa gac tta aca gag tat ctt aaa gtg agg tca cat 1229
Pro Asp Leu Ala Lys Asp Leu Thr Glu Tyr Leu Lys Val Arg Ser His
345 350 355 360

gac cct gag gaa gct att aga cat gat gtt att gtg tca ata gtt aca 1277
Asp Pro Glu Glu Ala Ile Arg His Asp Val Ile Val Ser Ile Val Thr
365 370 375

gct gct aaa aag gat att ctt ctg gtc aat gat cac tta ctt aat ttt 1325
Ala Ala Lys Lys Asp Ile Leu Leu Val Asn Asp His Leu Leu Asn Phe
380 385 390

gtg aga gag aga aca tta gac aaa cga tgg aga gta cgc aaa gaa gcc 1373
Val Arg Glu Arg Thr Leu Asp Lys Arg Trp Arg Val Arg Lys Glu Ala
395 400 405

atg atg gga ctt gcc caa att tat aag aaa tat gct tta cag tca gca 1421
Met Met Gly Leu Ala Gln Ile Tyr Lys Lys Tyr Ala Leu Gln Ser Ala
410 415 420

B1
gct gga aaa gat gct gca aaa cag ata gca tgg atc aaa gac aaa ttg 1469
Ala Gly Lys Asp Ala Ala Lys Gln Ile Ala Trp Ile Lys Asp Lys Leu
425 430 435 440

cta cat ata tat tat caa aat agt att gat gat cga cta ctt gtt gaa 1517
Leu His Ile Tyr Tyr Gln Asn Ser Ile Asp Asp Arg Leu Leu Val Glu
445 450 455

cgg atc ttt gct caa tac atg gtt cct cac aat tta gaa act aca gaa 1565
Arg Ile Phe Ala Gln Tyr Met Val Pro His Asn Leu Glu Thr Thr Glu
460 465 470

cgg atg aaa tgc tta tat tac ttg tat gcc aca ctg gat tta aat gct 1613
Arg Met Lys Cys Leu Tyr Tyr Leu Tyr Ala Thr Leu Asp Leu Asn Ala
475 480 485

gtg aaa gca ttg aat gaa atg tgg aaa tgt caa aat ctg ctc cga cat 1661
Val Lys Ala Leu Asn Glu Met Trp Lys Cys Gln Asn Leu Leu Arg His
490 495 500

caa gta aag gat ttg ctt gac ttg att aag caa ccc aaa aca gat gcc 1709
Gln Val Lys Asp Leu Leu Asp Leu Ile Lys Gln Pro Lys Thr Asp Ala
505 510 515 520

agt gtc aag gcc ata ttt tca aaa gtg atg gtt att aca aga aat tta 1757
Ser Val Lys Ala Ile Phe Ser Lys Val Met Val Ile Thr Arg Asn Leu
525 530 535

cct gat cct ggt aag gct cag gat ttc atg aag aaa ttc aca cag gtg	1805
Pro Asp Pro Gly Lys Ala Gln Asp Phe Met Lys Lys Phe Thr Gln Val	
540 545 550	
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Leu Glu Asp Asp Glu Lys Ile Arg Lys Gln Leu Glu Val Leu Val Ser	
555 560 565	
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Pro Thr Cys Ser Cys Lys Gln Ala Glu Gly Cys Val Arg Glu Ile Thr	
570 575 580	
aag aag ttg ggc aac ccc aaa cag cct aca aat cct ttc ctg gaa atg	1949
Lys Lys Leu Gly Asn Pro Lys Gln Pro Thr Asn Pro Phe Leu Glu Met	
585 590 600	
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Ile Lys Phe Leu Leu Glu Arg Ile Ala Pro Val His Ile Asp Thr Glu	
605 610 615	
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Ser Ile Ser Ala Leu Ile Lys Gln Val Asn Lys Ser Ile Asp Gly Thr	
620 625 630	
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Ala Asp Asp Glu Asp Glu Gly Val Pro Thr Asp Gln Ala Ile Arg Ala	
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Gly Leu Glu Leu Leu Lys Val Leu Ser Phe Thr His Pro Ile Ser Phe	
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His Ser Ala Glu Thr Phe Glu Ser Leu Leu Ala Cys Leu Lys Met Asp	
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Asp Glu Lys Val Ala Glu Ala Ala Leu Gln Ile Phe Lys Asn Thr Gly	
685 690 695	
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Ser Lys Ile Glu Glu Asp Phe Pro His Ile Arg Ser Ala Leu Leu Pro	
700 705 710	
gtt tta cat cac aaa tct aaa aaa gga ccc ccc cgt caa gcc aaa tat	2333
Val Leu His His Lys Ser Lys Lys Gly Pro Pro Arg Gln Ala Lys Tyr	
715 720 725	
gcc att cat tgt atc cat gcg ata ttt tct agt aaa gag acc cag ttt	2381
Ala Ile His Cys Ile His Ala Ile Phe Ser Ser Lys Glu Thr Gln Phe	
730 735 740	
gca cag ata ttt gag cct ctg cat aag agc cta gat cca agc aac ctg	2429
Ala Gln Ile Phe Glu Pro Leu His Lys Ser Leu Asp Pro Ser Asn Leu	
745 750 755 760	
gaa cat ctc ata aca cca ttg gtt act att ggt cat att gct ctc ctt	2477

Glu	His	Leu	Ile	Thr	Pro	Leu	Val	Thr	Ile	Gly	His	Ile	Ala	Leu	Leu	
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gca	cct	gat	caa	ttt	gct	gct	cct	tgg	aaa	tct	tgg	gta	gct	act	ttc	2525
Ala	Pro	Asp	Gln	Phe	Ala	Ala	Pro	Trp	Lys	Ser	Trp	Val	Ala	Thr	Phe	
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Ile	Val	Lys	Asp	Leu	Leu	Met	Asn	Asp	Arg	Leu	Pro	Gly	Lys	Lys	Thr	
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act	aaa	ctt	tgg	gtt	cca	gat	gaa	gaa	gta	tct	cct	gag	aca	atg	gtc	2621
Thr	Lys	Leu	Trp	Val	Pro	Asp	Glu	Glu	Val	Ser	Pro	Glu	Thr	Met	Val	
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aaa	att	cag	gct	att	aaa	atg	atg	gtt	cga	tgg	cta	ctt	gga	atg	aaa	2669
Lys	Ile	Gln	Ala	Ile	Lys	Met	Met	Val	Arg	Trp	Leu	Leu	Gly	Met	Lys	
825					830					835					840	
aat	aat	cac	agt	aaa	tca	gga	act	tct	acc	tta	aga	ttg	cta	aca	aca	2717
Asn	Asn	His	Ser	Lys	Ser	Gly	Thr	Ser	Thr	Leu	Arg	Leu	Leu	Thr	Thr	
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Ile	Leu	His	Ser	Asp	Gly	Asp	Leu	Thr	Glu	Gln	Gly	Lys	Ile	Ser	Lys	
			860					865					870			
cca	gat	atg	tca	cgt	ctg	aga	ctt	gct	gct	ggg	agt	gct	att	gtg	aag	2813
Pro	Asp	Met	Ser	Arg	Leu	Arg	Leu	Ala	Ala	Gly	Ser	Ala	Ile	Val	Lys	
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Leu	Ala	Gln	Glu	Pro	Cys	Tyr	His	Glu	Ile	Ile	Thr	Leu	Glu	Gln	Tyr	
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Gln	Leu	Cys	Ala	Leu	Ala	Ile	Asn	Asp	Glu	Cys	Tyr	Gln	Val	Arg	Gln	
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Val	Phe	Ala	Gln	Lys	Leu	His	Lys	Gly	Leu	Ser	Arg	Leu	Arg	Leu	Pro	
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Leu	Glu	Tyr	Met	Ala	Ile	Cys	Ala	Leu	Cys	Ala	Lys	Asp	Pro	Val	Lys	
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Glu	Arg	Arg	Ala	His	Ala	Arg	Gln	Cys	Leu	Val	Lys	Asn	Ile	Asn	Val	
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Arg	Arg	Glu	Tyr	Leu	Lys	Gln	His	Ala	Ala	Val	Ser	Glu	Lys	Leu	Leu	
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Ser	Leu	Leu	Pro	Glu	Tyr	Val	Val	Pro	Tyr	Thr	Ile	His	Leu	Leu	Ala	

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<220>
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Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr
1 5 10 15

ccg cct ggg gtc aag gaa ata tca gat aaa ata tct aaa gag gag atg 158
Pro Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met
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gtg aga cga tta aag atg gtt gtg aaa act ttt atg gat atg gac cag 206
Val Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln
35 40 45

gac tct gaa gaa gaa aag gag ctt tat tta aac cta gct tta cat ctt 254
Asp Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu
50 55 60

gct tca gat ttt ttt ctc aag cat cct gat aaa gat gtt cgc tta ctg 302
Ala Ser Asp Phe Phe Leu Lys His Pro Asp Lys Asp Val Arg Leu Leu
65 70 75

gta gcc tgc tgc ctt gct gat att ttc agg att tat gct cct gaa gct 350
Val Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala
80 85 90 95

cct tac aca tcc cct gat aaa cta aag gat ata ttt atg ttt ata aca 398
Pro Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr
100 105 110

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Arg Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg
115 120 125

tat ttt tat ttg ctt gag aac att gct tgg gtc aag tca tat aac ata 494
Tyr Phe Tyr Leu Leu Glu Asn Ile Ala Trp Val Lys Ser Tyr Asn Ile
130 135 140

tgc ttt gag tta gaa gat agc aat gaa att ttc acc cag cta tac aga 542
Cys Phe Glu Leu Glu Asp Ser Asn Glu Ile Phe Thr Gln Leu Tyr Arg
145 150 155

acc tta ttt tca gtt ata aac aat ggc cac aat cag aaa gtc cat atg 590
Thr Leu Phe Ser Val Ile Asn Asn Gly His Asn Gln Lys Val His Met
160 165 170 175

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His Met Val Asp Leu Met Ser Ser Ile Ile Cys Glu Gly Asp Thr Val
180 185 190

tct cag gag ctt ttg gat acg gtt tta gta aat ctg gta cct gct cat 686
Ser Gln Glu Leu Leu Asp Thr Val Leu Val Asn Leu Val Pro Ala His
195 200 205

aag aat tta aac aag caa gca tat gat ttg gca aag gct tta ctg aag 734
Lys Asn Leu Asn Lys Gln Ala Tyr Asp Leu Ala Lys Ala Leu Leu Lys

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tct gac tta att ttg gag ctc tac aat att gat agt cat ttg ctg ctc Ser Asp Leu Ile Leu Glu Leu Tyr Asn Ile Asp Ser His Leu Leu Leu 260 265 270			878
tct ggt tta ccc cag ctt gaa ttt aaa tta aag agc aat gat aat gag Ser Val Leu Pro Gln Leu Glu Phe Lys Leu Lys Ser Asn Asp Asn Glu 275 280 285			926
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gat tca gaa ttg gct tct caa aac aag cca ctt tgg cag tgc tac ttg Asp Ser Glu Leu Ala Ser Gln Asn Lys Pro Leu Trp Gln Cys Tyr Leu 305 310 315			1022
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Ile Phe Ser Ser Lys Glu Ala Gln Phe Ala Gln Ile Phe Glu Pro Leu	
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 Ser Asp Phe Phe Leu Lys His Pro Asp Lys Asp Val Arg Leu Leu Val
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 Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr Arg
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 Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg Tyr
 115 120 125
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 Phe Glu Leu Glu Asp Ser Asn Glu Ile Phe Thr Gln Leu Tyr Arg Thr
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 Thr Ala Gln Ala Ile Glu Pro Tyr Ile Thr Asn Phe Phe Asn Gln Val
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 Leu Met Leu Gly Lys Thr Ser Ile Ser Asp Leu Ser Glu His Val Ser
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 Val Leu Pro Gln Leu Glu Phe Lys Leu Lys Ser Asn Asp Asn Glu Glu
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Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val Leu		640
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Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu Ser		655
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	675	680
Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe Pro		685
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His Ile Arg Ser Ala Leu Leu Pro Val Leu His His Lys Ser Lys Lys		
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Gly Pro Pro Arg Gln Ala Lys Tyr Ala Ile His Cys Ile His Ala Ile		
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Lys Ser Leu Asp Pro Ser Asn Leu Glu His Leu Ile Thr Pro Leu Val		750
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Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys Val		990
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